

# BIO392-cnv-freq

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```
library(pgxRpi)

freq <- pgxLoader(type='frequency', output='pgxseg', filters = 'NCIT:C9245',
                  codematches = T)

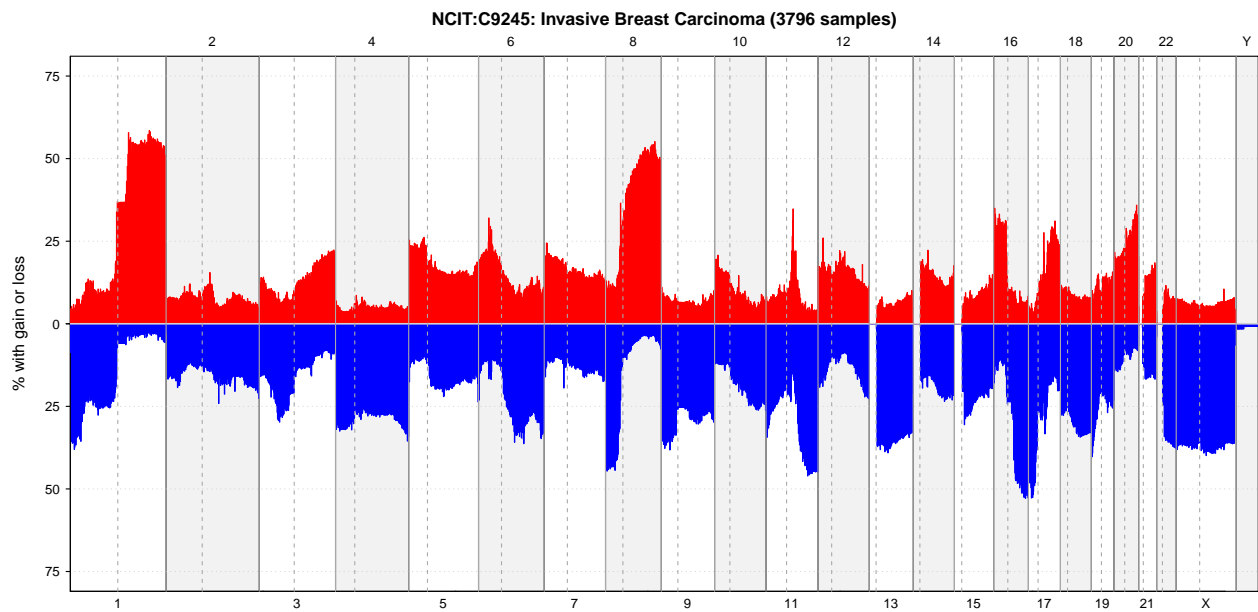
head(freq$data$'NCIT:C4025')

## NULL
```

## Step4: Visualize data

By genome

```
pgxFreqplot(freq)
```



## Step5: Analyse the data

p links, q rechts

According to the plot, we can see frequent gains on chromosome 1q,8q,16p,20q  
and frequent losses on 1p,8p,11q,16q,17p